

- 45 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: (Other than US) AMRAD OPERATIONS PTY LTD
(US only) Suzanne Cory, Jerry McKee Adams, Leonie Gibson and
Sean P Holmgreen

- (ii) TITLE OF INVENTION: ~~THERAPEUTIC MOLECULES~~
A Novel Mammalian Gene, bcl-w, belongs to the bcl-2
family of Apoptosis-controlling
genes.
- (iii) NUMBER OF SEQUENCES: 9

- (iv) ~~CORRESPONDENCE ADDRESS:~~
(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

- (v) ~~COMPUTER READABLE FORM:~~
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) ~~SOFTWARE: PatentIn Release #1.0, Version #1.25~~

- Prior*
(vi) ~~CURRENT~~ APPLICATION DATA:
(A) APPLICATION NUMBER: ~~PCT INTERNATIONAL~~ 09/155,327
(B) FILING DATE: 27-MAR-1997

- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PN 8965
(B) FILING DATE: 27-MAR-1996

- (viii) ~~ATTORNEY/AGENT INFORMATION:~~
(A) NAME: HUGHES DR, E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/EK

- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +61 3 9254 2777
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- 46 -

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTCTAGAAC TGGGG~~(A/C)~~G~~(A/G)~~ T~~(G/T)~~GCCTT ~~(C/T)~~TT
 n h n r n n y

33

wherein n is inosine at position 16, 19, 22 and 25.

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa
 Asn Trp Gly Arg ~~(Ile/Val)~~ Val Ala Phe Phe

5

wherein Xaa is Ile or Val.

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCCTCA GCC~~(C/T)~~T~~(G/T)~~ TCTTGGATCC A
 n n R n

31

wherein n is inosine at position 14, 17 and 20.

- 47 -

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ile Gln (~~Asp/Gln~~) (~~Asn/Gln~~) Gly Gly Trp
 Xaa 5 Xaa

wherein Xaa at position 4 is Asp or Glu, and Xaa at position 5 is Asn or Gln.

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val
 5 10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- 48 -

ATG	GCG	ACC	CCA	GCC	TCG	GCC	CCA	GAC	ACA	CGG	GCT	CTG	GTG	GCA	GAC	48
Met	Ala	Thr	Pro	Ala	Ser	Ala	Pro	Asp	Thr	Arg	Ala	Leu	Val	Ala	Asp	
1				5				10						15		
TTT	GTA	GGT	TAT	AAG	CTG	AGG	CAG	AAG	GGT	TAT	GTC	TGT	GGA	GCT	GGC	96
Phe	Val	Gly	Tyr	Lys	Leu	Arg	Gln	Lys	Gly	Tyr	Val	Cys	Gly	Ala	Gly	
			20					25					30			
CCC	GGG	GAG	GGC	CCA	GCA	GCT	GAC	CCG	CTG	CAC	CAA	GCC	ATG	CGG	GCA	144
Pro	Gly	Glu	Gly	Pro	Ala	Ala	Asp	Pro	Leu	His	Gln	Ala	Met	Arg	Ala	
		35					40					45				
GCT	GGA	GAT	GAG	TTC	GAG	ACC	CGC	TTC	CGG	CGC	ACC	TTC	TCT	GAT	CTG	192
Ala	Gly	Asp	Glu	Phe	Glu	Thr	Arg	Phe	Arg	Arg	Thr	Phe	Ser	Asp	Leu	
	50					55					60					
GCG	GCT	CAG	CTG	CAT	GTG	ACC	CCA	GGC	TCA	GCC	CAG	CAA	CGC	TTC	ACC	240
Ala	Ala	Gln	Leu	His	Val	Thr	Pro	Gly	Ser	Ala	Gln	Gln	Arg	Phe	Thr	
65					70					75					80	
CAG	GTC	TCC	GAC	GAA	CTT	TTT	CAA	GGG	GGC	CCC	AAC	TGG	GGC	CGC	CTT	288
Gln	Val	Ser	Asp	Glu	Leu	Phe	Gln	Gly	Gly	Pro	Asn	Trp	Gly	Arg	Leu	
				85				90						95		
GTA	GCC	TTC	TTT	CTC	TTT	GGG	GCT	GCA	CTG	TGT	GCT	GAG	AGT	GTC	AAC	336
Val	Ala	Phe	Phe	Leu	Phe	Gly	Ala	Ala	Leu	Cys	Ala	Glu	Ser	Val	Asn	
			100	Val			105						110			
AAG	GAG	ATG	GAA	CCA	CTG	GTG	GGA	CAA	GTG	CAG	GAG	TGG	ATG	GTG	GCC	384
Lys	Glu	Met	Glu	Pro	Leu	Val	Gly	Gln	Val	Gln	Glu	Trp	Met	Val	Ala	
		115					120					125				
TAC	CTG	GAG	ACG	CGG	CTG	GTC	GAC	TGG	ATC	CAC	AGC	AGT	GGG	GGC	TGG	432
Tyr	Leu	Glu	Thr	Arg	Leu	Val	Asp	Trp	Ile	His	Ser	Ser	Gly	Gly	Trp	
	130					135					140					
GCG	GAG	TTC	ACA	GCT	CTA	TAC	GGG	GAC	GGG	GCC	CTG	GAG	GAG	GCG	CGG	480
Ala	Glu	Phe	Thr	Ala	Leu	Tyr	Gly	Asp	Gly	Ala	Leu	Glu	Glu	Ala	Arg	
145					150					155					160	
CGT	CTG	CGG	GAG	GGG	AAC	TGG	GCA	TCA	GTG	AGG	ACA	GTG	CTG	ACG	GGG	528
Arg	Leu	Arg	Glu	Gly	Asn	Trp	Ala	Ser	Val	Arg	Thr	Val	Leu	Thr	Gly	
				165					170					175		
GCC	GTG	GCA	CTG	GGG	GCC	CTG	GTA	ACT	GTA	GGG	GCC	TTT	TTT	GCT	AGC	576
Ala	Val	Ala	Leu	Gly	Ala	Leu	Val	Thr	Val	Gly	Ala	Phe	Phe	Ala	Ser	
			180				185					190				
AAG	TGA	A														583
Lys	*															

- 49 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Thr Pro Ala Ser Ala Pro Asp Thr Arg Ala Leu Val Ala Asp
 1 5 10 15

Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95

Val Ala Phe Phe ^{Val}~~Leu~~ Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
 115 120 125

Tyr Leu Glu Thr Arg Leu ^{Ala}~~Val~~ Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190

Lys *

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

- 50 -

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	CCG	ACC	CCA	GCC	TCA	ACC	CCA	GAC	ACA	CG	GCT	CTA	GTG	GCT	GAC	48
Met	Pro	Thr	Pro	Ala	Ser	Thr	Pro	Asp	Thr	Arg	Ala	Leu	Val	Ala	Asp	
1	Ala			5				10						15		
TTT	GTA	GGC	TAT	AGG	CTG	AGG	CAG	AAG	GGT	TAT	GTC	TGT	GGA	GCT	GG	96
Phe	Val	Gly	Tyr	Arg	Leu	Arg	Gln	Lys	Gly	Tyr	Val	Cys	Gly	Ala	Gly	
		20					25					30				
CCT	GGG	GAA	GGC	CCA	GCC	GCC	GAC	CCG	CTG	CAC	CAA	GCC	ATG	CGG	GCT	144
Pro	Gly	Glu	Gly	Pro	Ala	Ala	Asp	Pro	Leu	His	Gln	Ala	Met	Arg	Ala	
		35					40					45				
GCT	GGA	GAC	GAG	TTT	GAG	ACC	CGT	TTC	CGC	CGC	ACC	TTC	TCT	GAC	CTG	192
Ala	Gly	Asp	Glu	Phe	Glu	Thr	Arg	Phe	Arg	Arg	Thr	Phe	Ser	Asp	Leu	
	50					55					60					
GCC	GCT	CAG	CTA	CAC	GTG	ACC	CCA	GGC	TCA	GCC	CAG	CAA	CGC	TTC	ACC	240
Ala	Ala	Gln	Leu	His	Val	Thr	Pro	Gly	Ser	Ala	Gln	Gln	Arg	Phe	Thr	
	65				70				75					80		
CAG	GTT	TCC	GAC	GAA	CTT	TTC	CAA	GGG	GGC	CCT	AAC	TGG	GGC	CGT	CTT	288
Gln	Val	Ser	Asp	Glu	Leu	Phe	Gln	Gly	Gly	Pro	Asn	Trp	Gly	Arg	Leu	
			85					90					95			
GTG	GCA	TTC	TTT	GTC	TTT	GGG	GCT	GCC	CTG	TGT	GCT	GAG	AGT	GTC	AAC	336
Val	Ala	Phe	Phe	Val	Phe	Gly	Ala	Ala	Leu	Cys	Ala	Glu	Ser	Val	Asn	
		100					105					110				
AAA	GAA	ATG	GAG	CCT	TTG	GTG	GGA	CAA	GT	CAG	GAT	TGG	AT	GTG	GCC	384
Lys	Glu	Met	Glu	Pro	Leu	Val	Gly	Gln	Val	Gln	Asp	Trp	Ile	Val	Ala	
	115						120					125	Met			
TAC	CTG	GAG	ACA	CGT	CTG	GCT	GAC	TGG	ATC	CAC	AGC	AGT	GGC	GGC	TGG	432
Tyr	Leu	Glu	Thr	Arg	Leu	Ala	Asp	Trp	Ile	His	Ser	Ser	Gly	Gly	Trp	
	130					135					140					
GCG	GAT	TTC	ACA	GCT	CTA	TAC	GGG	GAC	GGG	GCC	CTG	GAG	GAT	GCA	CGG	480
Ala	Asp	Phe	Thr	Ala	Leu	Tyr	Gly	Asp	Gly	Ala	Leu	Glu	Asp	Ala	Arg	
145	Glu				150				155			Glu		160		
CGT	CTG	CGG	GAG	GG	AAC	TGG	GCA	TGA	GTG	AG	ACA	GTG	GTG	ACG	GGG	528
Arg	Leu	Arg	Glu	Gly	Asn	Trp	Ala	Val	Ser	Val	Thr	Val	Val	Thr	Gly	
			165					170	Arg				Leu	175		
GCC	GTG	GCA	CTG	GGG	GCC	CTG	GTA	ACT	GTA	GGG	GCC	TTT	TTT	GCT	AGC	576

- 51 -

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190

AAG TGA
 Lys

582

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met ^{Ala}~~Pro~~ Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
 1 5 10 15

Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30

Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp ^{Met}~~He~~ Val Ala
 115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140

Ala ^{Glu}~~Asp~~ Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu ^{Glu}~~Asp~~ Ala Arg
 145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala ^{Ser}~~Val~~ Val ^{Arg}~~Ser~~ Thr Val ^{Leu}~~Val~~ Thr Gly
 165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
 180 185 190

Lys